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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gray, Patrick W.  
Schweickart, Vicky L.  
Raport, Carol J.
- (ii) TITLE OF INVENTION: Chemokine Receptor Materials and Methods
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 S. Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: USA
  - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Noland, Greta E.
  - (B) REGISTRATION NUMBER: 35,302
  - (C) REFERENCE/DOCKET NUMBER: 27866/33670
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 312-474-6300
  - (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 55..1110
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: /= "88C polynucleotide and amino acid sequences"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAG ATG  
Met

1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAT | TAT | CAA | GTG | TCA | AGT | CCA | ATC | TAT | GAC | ATC | AAT | TAT | TAT | ACA | TCG | 105 |
| Asp | Tyr | Gln | Val | Ser | Ser | Pro | Ile | Tyr | Asp | Ile | Asn | Tyr | Tyr | Thr | Ser |     |
|     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| GAG | CCC | TGC | CAA | AAA | ATC | AAT | GTG | AAG | CAA | ATC | GCA | GCC | CGC | CTC | CTG | 153 |
| Glu | Pro | Cys | Gln | Lys | Ile | Asn | Val | Lys | Gln | Ile | Ala | Ala | Arg | Leu | Leu |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |     |
| CCT | CCG | CTC | TAC | TCA | CTG | GTG | TTC | ATC | TTT | GGT | TTT | GTG | GGC | AAC | ATG | 201 |
| Pro | Pro | Leu | Tyr | Ser | Leu | Val | Phe | Ile | Phe | Gly | Phe | Val | Gly | Asn | Met |     |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| CTG | GTC | ATC | CTC | ATC | CTG | ATA | AAC | TGC | AAA | AGG | CTG | AAG | AGC | ATG | ACT | 249 |
| Leu | Val | Ile | Leu | Ile | Leu | Ile | Asn | Cys | Lys | Arg | Leu | Lys | Ser | Met | Thr |     |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |
| GAC | ATC | TAC | CTG | CTC | AAC | CTG | GCC | ATC | TCT | GAC | CTG | TTT | TTC | CTT | CTT | 297 |
| Asp | Ile | Tyr | Leu | Leu | Asn | Leu | Ala | Ile | Ser | Asp | Leu | Phe | Phe | Leu | Leu |     |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| ACT | GTC | CCC | TTC | TGG | GCT | CAC | TAT | GCT | GCC | GCC | CAG | TGG | GAC | TTT | GGA | 345 |
| Thr | Val | Pro | Phe | Trp | Ala | His | Tyr | Ala | Ala | Ala | Gln | Trp | Asp | Phe | Gly |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| AAT | ACA | ATG | TGT | CAA | CTC | TTG | ACA | GGG | CTC | TAT | TTT | ATA | GGC | TTC | TTC | 393 |
| Asn | Thr | Met | Cys | Gln | Leu | Leu | Thr | Gly | Leu | Tyr | Phe | Ile | Gly | Phe | Phe |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |
| TCT | GGA | ATC | TTC | TTC | ATC | ATC | CTC | CTG | ACA | ATC | GAT | AGG | TAC | CTG | GCT | 441 |
| Ser | Gly | Ile | Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | Ala |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| GTC | GTC | CAT | GCT | GTG | TTT | GCT | TTA | AAA | GCC | AGG | ACG | GTC | ACC | TTT | GGG | 489 |
| Val | Val | His | Ala | Val | Phe | Ala | Leu | Lys | Ala | Arg | Thr | Val | Thr | Phe | Gly |     |
|     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     | 145 |     |
| GTG | GTG | ACA | AGT | GTG | ATC | ACT | TGG | GTG | GTG | GCT | GTG | TTT | GCG | TCT | CTC | 537 |
| Val | Val | Thr | Ser | Val | Ile | Thr | Trp | Val | Val | Ala | Val | Phe | Ala | Ser | Leu |     |
|     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |     |
| CCA | GGA | ATC | ATC | TTT | ACC | AGA | TCT | CAA | AAA | GAA | GGT | CTT | CAT | TAC | ACC | 585 |
| Pro | Gly | Ile | Ile | Phe | Thr | Arg | Ser | Gln | Lys | Glu | Gly | Leu | His | Tyr | Thr |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |
| TGC | AGC | TCT | CAT | TTT | CCA | TAC | AGT | CAG | TAT | CAA | TTC | TGG | AAG | AAT | TTC | 633 |
| Cys | Ser | Ser | His | Phe | Pro | Tyr | Ser | Gln | Tyr | Gln | Phe | Trp | Lys | Asn | Phe |     |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |
| CAG | ACA | TTA | AAG | ATA | GTC | ATC | TTG | GGG | CTG | GTC | CTG | CCG | CTG | CTT | GTC | 681 |
| Gln | Thr | Leu | Lys | Ile | Val | Ile | Leu | Gly | Leu | Val | Leu | Pro | Leu | Leu | Val |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |
| ATG | GTC | ATC | TGC | TAC | TCG | GGA | ATC | CTA | AAA | ACT | CTG | CTT | CGG | TGT | CGA | 729 |
| Met | Val | Ile | Cys | Tyr | Ser | Gly | Ile | Leu | Lys | Thr | Leu | Leu | Arg | Cys | Arg |     |
|     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     | 225 |     |     |
| AAT | GAG | AAG | AAG | AGG | CAC | AGG | GCT | GTG | AGG | CTT | ATC | TTC | ACC | ATC | ATG | 777 |
| Asn | Glu | Lys | Lys | Arg | His | Arg | Ala | Val | Arg | Leu | Ile | Phe | Thr | Ile | Met |     |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |
| ATT | GTT | TAT | TTT | CTC | TTC | TGG | GCT | CCC | TAC | AAC | ATT | GTC | CTT | CTC | CTG | 825 |
| Ile | Val | Tyr | Phe | Leu | Phe | Trp | Ala | Pro | Tyr | Asn | Ile | Val | Leu | Leu | Leu |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |
| AAC | ACC | TTC | CAG | GAA | TTC | TTT | GGC | CTG | AAT | AAT | TGC | AGT | AGC | TCT | AAC | 873 |
| Asn | Thr | Phe | Gln | Glu | Phe | Phe | Gly | Leu | Asn | Asn | Cys | Ser | Ser | Ser | Asn |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |

|             |         |        |        |        |         |          |        |         |        |         |     |     |     |     |     |      |
|-------------|---------|--------|--------|--------|---------|----------|--------|---------|--------|---------|-----|-----|-----|-----|-----|------|
| AGG         | TTG     | GAC    | CAA    | GCT    | ATG     | CAG      | GTG    | ACA     | GAG    | ACT     | CTT | GGG | ATG | ACG | CAC | 921  |
| Arg         | Leu     | Asp    | Gln    | Ala    | Met     | Gln      | Val    | Thr     | Glu    | Thr     | Leu | Gly | Met | Thr | His |      |
|             | 275     |        |        |        |         | 280      |        |         |        |         | 285 |     |     |     |     |      |
| TGC         | TGC     | ATC    | AAC    | CCC    | ATC     | ATC      | TAT    | GCC     | TTT    | GTC     | GGG | GAG | AAG | TTC | AGA | 969  |
| Cys         | Cys     | Ile    | Asn    | Pro    | Ile     | Ile      | Tyr    | Ala     | Phe    | Val     | Gly | Glu | Lys | Phe | Arg |      |
|             | 290     |        |        |        | 295     |          |        |         |        | 300     |     |     |     |     | 305 |      |
| AAC         | TAC     | CTC    | TTA    | GTC    | TTC     | TTC      | CAA    | AAG     | CAC    | ATT     | GCC | AAA | CGC | TTC | TGC | 1017 |
| Asn         | Tyr     | Leu    | Leu    | Val    | Phe     | Phe      | Gln    | Lys     | His    | Ile     | Ala | Lys | Arg | Phe | Cys |      |
|             |         |        |        | 310    |         |          |        |         | 315    |         |     |     |     | 320 |     |      |
| AAA         | TGC     | TGT    | TCT    | ATT    | TTC     | CAG      | CAA    | GAG     | GCT    | CCC     | GAG | CGA | GCA | AGC | TCA | 1065 |
| Lys         | Cys     | Cys    | Ser    | Ile    | Phe     | Gln      | Gln    | Glu     | Ala    | Pro     | Glu | Arg | Ala | Ser | Ser |      |
|             |         |        | 325    |        |         |          |        | 330     |        |         |     |     | 335 |     |     |      |
| GTT         | TAC     | ACC    | CGA    | TCC    | ACT     | GGG      | GAG    | CAG     | GAA    | ATA     | TCT | GTG | GGC | TTG |     | 1110 |
| Val         | Tyr     | Thr    | Arg    | Ser    | Thr     | Gly      | Glu    | Gln     | Glu    | Ile     | Ser | Val | Gly | Leu |     |      |
|             |         | 340    |        |        |         | 345      |        |         |        |         |     | 350 |     |     |     |      |
| TGACACGGAC  | TCAAGTG | GGGC   | TGGTG  | ACCCA  | GTCAG   | AGTTG    | TGCAC  | ATGGC   | TTAGT  | TTTTCA  |     |     |     |     |     | 1170 |
| TACACAGCCT  | GGGCTG  | GGGG   | TGGGGT | GGGA   | GAGGTCT | TTTT     | TTAA   | AAGGAA  | GTTACT | GTTA    |     |     |     |     |     | 1230 |
| TAGAGGGTCT  | AAGATT  | CATC   | CATT   | TATTTG | GCATCT  | GTTT     | AAAG   | TAGATT  | AGATCT | TTTTA   |     |     |     |     |     | 1290 |
| AGCCCCATCAA | TTATAG  | AAAAG  | CCAAAT | CAAA   | ATATG   | TTGAT    | GAAAA  | ATAGC   | AACCT  | TTTTTA  |     |     |     |     |     | 1350 |
| TCTCCCCCTTC | ACATGC  | CATCA  | AGTT   | TATGAC | AAACT   | CTCCCC   | TTC    | ACTCCGA | AAGTT  | CCTTA   |     |     |     |     |     | 1410 |
| TGTATATTTTA | AAAGAA  | AGCC   | TCAG   | AGAATT | GCTG    | ATTCTT   | GAGTT  | TAGTG   | ATCT   | GAAACAG |     |     |     |     |     | 1470 |
| AAATACCAAAA | ATTATTT | TCAG   | AAAT   | GTACAA | CTTTTT  | TACCT    | AGT    | ACAAGGC | AAC    | ATATAGG |     |     |     |     |     | 1530 |
| TTGTAAATGT  | GTTTAAA | ACA    | GGTCT  | TTTGTC | TTGCT   | ATGGG    | GAGAA  | AAGAC   | ATGA   | ATATGA  |     |     |     |     |     | 1590 |
| TTAGTAAAGA  | AATGAC  | ACTT   | TTCAT  | GTGTG  | ATTT    | CCCCCTC  | CAAGG  | TATGG   | TTAATA | AGTT    |     |     |     |     |     | 1650 |
| TCACTGACTT  | AGAACC  | CAGGC  | GAGAG  | ACTTG  | TGGCCT  | TGGGA    | GAGCT  | TGGGA   | AGCTT  | CTTAA   |     |     |     |     |     | 1710 |
| ATGAGAAGGA  | ATTTG   | AGTTG  | GATCAT | CTAT   | TGCTG   | GCAAA    | GACAG  | AAGCC   | TCACT  | GCAAG   |     |     |     |     |     | 1770 |
| CACTGCATGG  | GCAAGC  | TTGG   | CTGT   | AGAAG  | AGAC    | CAGAGCT  | GGTT   | TGGGAAG | ACAT   | TGGGGAG |     |     |     |     |     | 1830 |
| GAAGGACAAG  | GCTAG   | ATCAT  | GAAGA  | ACCTT  | GACGG   | CATTG    | CTCCG  | TCTAA   | GTCAT  | GAGCT   |     |     |     |     |     | 1890 |
| GAGCAGGGAG  | ATCCT   | TGGTTG | GTGTT  | GCAGA  | AGGTTT  | ACTC     | TGTG   | GCCAAA  | GGAGG  | GTGAG   |     |     |     |     |     | 1950 |
| GAAGGATGAG  | CATTT   | AGGGC  | AAGG   | AGACCA | CCAAC   | AGCCC    | TCAGG  | TCAGG   | GTGAG  | GATGG   |     |     |     |     |     | 2010 |
| CCTCTGCTAA  | GCTCA   | AGGCG  | TGAGG  | ATGGG  | AAGG    | AGGGAG   | GTATT  | TCGTAA  | GGAT   | TGGGAAG |     |     |     |     |     | 2070 |
| GAGGGAGGTA  | TTCTG   | TCAGC  | ATATG  | AGGAT  | GCAG    | AGTCAG   | CAGAA  | CTGGG   | GTGG   | ATTTGG  |     |     |     |     |     | 2130 |
| TTTGGAAGTG  | AGGGT   | CAGAG  | AGGAG  | TCAGA  | GAGA    | ATCCCT   | AGTCT  | TTCAAG  | CAGAT  | TGGAG   |     |     |     |     |     | 2190 |
| AAACCCCTTGA | AAAG    | CATCA  | AGCAC  | AGAAG  | GAGG    | AGGAGG   | AGGTTT | TAGGT   | CAAGA  | AAGAAG  |     |     |     |     |     | 2250 |
| ATGGATTGGT  | GTAAA   | AGGAT  | GGGT   | CTGGTT | TGC     | CAGAGCTT | GAAC   | CAGTC   | TCAC   | CCAGAC  |     |     |     |     |     | 2310 |
| TCCAGGCTGT  | CTTT    | CACTGA | ATGCT  | TCTGA  | CTT     | CATAGAT  | TTCTT  | TCCCA   | TCCC   | CAGCTGA |     |     |     |     |     | 2370 |
| AATACTGAGG  | GGTCT   | CCAGG  | AGG    | GACTAG | ATTT    | TATGAAT  | ACAC   | GAGGTA  | TGAG   |         |     |     |     |     |     |      |

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TTCAATAAGC ATCAAACCTCT TAGTTACTCA TTCAGGGATA GCACTGAGCA AAGCATTGAG 2610
CAAAGGGGTC CCATATAGGT GAGGGAAGCC TGAAAACTA AGATGCTGCC TGCCCAGTGC 2670
ACACAAGTGT AGGTATCATT TTCTGCATTT AACCGTCAAT AGGCAAAGGG GGGAAAGGGAC 2730
ATATTCATTT GGAAATAAGC TGCCTTGAGC CTTAAAACCC ACAAAGTAC AATTTACCAG 2790
CCTCCGTATT TCAGACTGAA TGGGGGTGGG GGGGGCGCCT TAGGTACTTA TTCCAGATGC 2850
CTTCTCCAGA CAAACCAGAA GCAACAGAAA AAATCGTCTC TCCCTCCCTT TGAAATGAAT 2910
ATACCCCTTA GTGTTTGGGT ATATTCATTT CAAAGGGAGA GAGAGAGGTT TTTTCTGT 2970
CTTTCTCATA TGATTGTGCA CATACTTGAG ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC 3030
CATCATAGTA CAGGTAAGGT GAGGGAATAG TAAGTGGTGA GAACTACTCA GGGAAATGAAG 3090
GTGTCAGAAT AATAAGAGGT GCTACTGACT TTCTCAGCCT CTGAATATGA ACGGTGAGCA 3150
TTGTGGCTGT CAGCAGGAAG CAACGAAGGG AAATGTCTTT CCTTTTGCTC TTAAGTTGTG 3210
GAGAGTGCAA CAGTAGCATA GGACCCTACC CTCTGGGCCA AGTCAAAGAC ATTCTGACAT 3270
CTTAGTATTT GCATATTCTT ATGTATGTGA AAGTTACAAA TTGCTTGAAA GAAAATATGC 3330
ATCTAATAAA AAACACCTTC TAAATAAAA AAAAAAAAAA AAAAAAAAAA AAA 3383

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: /= "88C amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1          5          10          15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20          25          30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35          40          45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50          55          60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65          70          75          80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85          90          95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100          105          110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115          120          125

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Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe  
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser  
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr  
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn  
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 362..1426

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /= "88-2B polynucleotide and amino acid sequences"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATAATAATGA TTATTATATT GTTATCATTA TCTAGCCTGT TTTTTCCTGT TTTGTATTTT 60

TTCCTTTTAAA TGCTTTTCAGA AATCTGTATC CCCATTCTTC ACCACCACCC CACAACATTT 120

|   |      |
|---|------|
| CTGCTTCTTT TCCCATGCCG GGTCATGCTA ACTTTGAAAG CTTCAGCTCT TTCCTTCCTC | 180  |
| AATCCTTTTC CTGGCACCTC TGATATGCCT TTTGAAATTC ATGTTAAAGA ATCCCTAGGC | 240  |
| TGCTATCACA TGTGGCATCT TTGTTGAGTA CATGAATAAA TCAACTGGTG TGTTTTACGA | 300  |
| AGGATGATTA TGCTTCATTG TGGGATTGTA TTTTCTTCT TCTATCACAG GGAGAAGTGA  | 360  |
| A ATG ACA ACC TCA CTA GAT ACA GTT GAG ACC TTT GGT ACC ACA TCC     | 406  |
| Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser       |      |
| 1 5 10 15   |      |
| TAC TAT GAT GAC GTG GGC CTG CTC TGT GAA AAA GCT GAT ACC AGA GCA   | 454  |
| Tyr Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala   |      |
| 20 25 30  |      |
| CTG ATG GCC CAG TTT GTG CCC CCG CTG TAC TCC CTG GTG TTC ACT GTG   | 502  |
| Leu Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val   |      |
| 35 40 45  |      |
| GGC CTC TTG GGC AAT GTG GTG GTG GTG ATG ATC CTC ATA AAA TAC AGG   | 550  |
| Gly Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg   |      |
| 50 55 60  |      |
| AGG CTC CGA ATT ATG ACC AAC ATC TAC CTG CTC AAC CTG GCC ATT TCG   | 598  |
| Arg Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser   |      |
| 65 70 75  |      |
| GAC CTG CTC TTC CTC GTC ACC CTT CCA TTC TGG ATC CAC TAT GTC AGG   | 646  |
| Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg   |      |
| 80 85 90 95   |      |
| GGG CAT AAC TGG GTT TTT GGC CAT GGC ATG TGT AAG CTC CTC TCA GGG   | 694  |
| Gly His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly   |      |
| 100 105 110   |      |
| TTT TAT CAC ACA GGC TTG TAC AGC GAG ATC TTT TTC ATA ATC CTG CTG   | 742  |
| Phe Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu   |      |
| 115 120 125   |      |
| ACA ATC GAC AGG TAC CTG GCC ATT GTC CAT GCT GTG TTT GCC CTT CGA   | 790  |
| Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg   |      |
| 130 135 140   |      |
| GCC CGG ACT GTC ACT TTT GGT GTC ATC ACC AGC ATC GTC ACC TGG GGC   | 838  |
| Ala Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly   |      |
| 145 150 155   |      |
| CTG GCA GTG CTA GCA GCT CTT CCT GAA TTT ATC TTC TAT GAG ACT GAA   | 886  |
| Leu Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu   |      |
| 160 165 170 175   |      |
| GAG TTG TTT GAA GAG ACT CTT TGC AGT GCT CTT TAC CCA GAG GAT ACA   | 934  |
| Glu Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr   |      |
| 180 185 190   |      |
| GTA TAT AGC TGG AGG CAT TTC CAC ACT CTG AGA ATG ACC ATC TTC TGT   | 982  |
| Val Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys   |      |
| 195 200 205   |      |
| CTC GTT CTC CCT CTG CTC GTT ATG GCC ATC TGC TAC ACA GGA ATC ATC   | 1030 |
| Leu Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile   |      |
| 210 215 220   |      |
| AAA ACG CTG CTG AGG TGC CCC AGT AAA AAA AAG TAC AAG GCC ATC CGG   | 1078 |
| Lys Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg   |      |
| 225 230 235   |      |

|             |            |            |             |             |             |            |            |     |     |     |     |     |     |     |     |      |
|-------------|------------|------------|-------------|-------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CTC         | ATT        | TTT        | GTC         | ATC         | ATG         | GCG        | GTG        | TTT | TTC | ATT | TTC | TGG | ACA | CCC | TAC | 1126 |
| Leu         | Ile        | Phe        | Val         | Ile         | Met         | Ala        | Val        | Phe | Phe | Ile | Phe | Trp | Thr | Pro | Tyr |      |
| 240         |            |            |             |             | 245         |            |            |     |     | 250 |     |     |     |     | 255 |      |
| AAT         | GTG        | GCT        | ATC         | CTT         | CTC         | TCT        | TCC        | TAT | CAA | TCC | ATC | TTA | TTT | GGA | AAT | 1174 |
| Asn         | Val        | Ala        | Ile         | Leu         | Leu         | Ser        | Ser        | Tyr | Gln | Ser | Ile | Leu | Phe | Gly | Asn |      |
|             |            |            |             | 260         |             |            |            |     | 265 |     |     |     |     | 270 |     |      |
| GAC         | TGT        | GAG        | CGG         | AGC         | AAG         | CAT        | CTG        | GAC | CTG | GTC | ATG | CTG | GTG | ACA | GAG | 1222 |
| Asp         | Cys        | Glu        | Arg         | Ser         | Lys         | His        | Leu        | Asp | Leu | Val | Met | Leu | Val | Thr | Glu |      |
|             |            |            | 275         |             |             |            |            | 280 |     |     |     |     | 285 |     |     |      |
| GTG         | ATC        | GCC        | TAC         | TCC         | CAC         | TGC        | TGC        | ATG | AAC | CCG | GTG | ATC | TAC | GCC | TTT | 1270 |
| Val         | Ile        | Ala        | Tyr         | Ser         | His         | Cys        | Cys        | Met | Asn | Pro | Val | Ile | Tyr | Ala | Phe |      |
|             |            | 290        |             |             |             |            | 295        |     |     |     |     | 300 |     |     |     |      |
| GTT         | GGA        | GAG        | AGG         | TTC         | CGG         | AAG        | TAC        | CTG | CGC | CAC | TTC | TTC | CAC | AGG | CAC | 1318 |
| Val         | Gly        | Glu        | Arg         | Phe         | Arg         | Lys        | Tyr        | Leu | Arg | His | Phe | Phe | His | Arg | His |      |
|             | 305        |            |             |             |             | 310        |            |     |     |     | 315 |     |     |     |     |      |
| TTG         | CTC        | ATG        | CAC         | CTG         | GGC         | AGA        | TAC        | ATC | CCA | TTC | CTT | CCT | AGT | GAG | AAG | 1366 |
| Leu         | Leu        | Met        | His         | Leu         | Gly         | Arg        | Tyr        | Ile | Pro | Phe | Leu | Pro | Ser | Glu | Lys |      |
| 320         |            |            |             |             | 325         |            |            |     | 330 |     |     |     |     |     | 335 |      |
| CTG         | GAA        | AGA        | ACC         | AGC         | TCT         | GTC        | TCT        | CCA | TCC | ACA | GCA | GAG | CCG | GAA | CTC | 1414 |
| Leu         | Glu        | Arg        | Thr         | Ser         | Ser         | Val        | Ser        | Pro | Ser | Thr | Ala | Glu | Pro | Glu | Leu |      |
|             |            |            |             | 340         |             |            |            |     | 345 |     |     |     |     | 350 |     |      |
| TCT         | ATT        | GTG        | TTT         | TAGGTCAGAT  | GCAGAAAATT  | GCCTAAAGAG | GAAGGACCAA |     |     |     |     |     |     |     |     | 1466 |
| Ser         | Ile        | Val        | Phe         |             |             |            |            |     |     |     |     |     |     |     |     |      |
|             |            |            | 355         |             |             |            |            |     |     |     |     |     |     |     |     |      |
| GGAGATGAAG  | CAAACACATT | AAGCCTTCCA | CACTCACCTC  | TAAAACAGTC  | CTTCAAACCTT |            |            |     |     |     |     |     |     |     |     | 1526 |
| CCAGTGCAAC  | ACTGAAGCTC | TTGAAGACAC | TGAAATATAC  | ACACAGCAGT  | AGCAGTAGAT  |            |            |     |     |     |     |     |     |     |     | 1586 |
| GCGATGTACCC | TAAGGTCATT | ACCACAGGCC | AGGGGCTGGG  | CAGCGTACTC  | ATCATCAACC  |            |            |     |     |     |     |     |     |     |     | 1646 |
| CTAAAAAGCA  | GAGCTTTGCT | TCTCTCTCTA | AAATGAGTTA  | CCTACATTTT  | AATGCACCTG  |            |            |     |     |     |     |     |     |     |     | 1706 |
| AATGTTAGAT  | AGTTACTATA | TGCCGCTACA | AAAAGGTAAA  | ACTTTTTTATA | TTTTATACAT  |            |            |     |     |     |     |     |     |     |     | 1766 |
| TAACTTCAGC  | CAGCTATTGA | TATAAATAAA | ACATTTTTCAC | ACAATACAAT  | AAGTTAACTA  |            |            |     |     |     |     |     |     |     |     | 1826 |
| TTTTATTTTC  | TAATGTGCCT | AGTTCTTTCC | CTGCTTAATG  | AAAAGCTTGT  | TTTTTCAGTG  |            |            |     |     |     |     |     |     |     |     | 1886 |
| TGAATAAATA  | ATCGTAAGCA | ACAAAAAAA  |             |             |             |            |            |     |     |     |     |     |     |     |     | 1915 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /= "88-2B amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Ser | Leu | Asp | Thr | Val | Glu | Thr | Phe | Gly | Thr | Thr | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |



[illegible]

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: /= "V28degf2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGGATCCA TYGAYAGRTA CCTGGCYATY GTCC

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: /= "V28degr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTAAGCTTT TRTAGGGDGT CCAYAAGAGY AA

32

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: /= "88c-r4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATAAGCCTC ACAGCCCTGT G

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: /= "88c-rlb"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTAAGCTTG ATGACTATCT TTAATGTC

28

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88-2B-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCTCTAGAC TAAACACAA TAGAGAG

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88-2B-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTAAGCTTA TCACAGGGAG AAGTGAAATG

30

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88-2B-f1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTGCTAGCA GCTCTTCCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88-2B-r1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCAGCGTT TTGATGATTC

20

- (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88C-f1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGTTTGCT TTAAAAGCC

19

- (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "88C-r3"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAGCCTCAC AGCCCTG

17

- (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: /= "CCCKR1(2)-5' Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGTAAGCTTA GAGAAGCCGG GATGGGAA

28

- (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: /= "CCCKR-3' Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCTCTAGAG TCAGAGACCA GCAGA

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACAAGCTTC ACAGGGTGGA ACAAGATG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTCTCTAGAC CACTTGAGTC CGTGTCA

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| ATG<br>Met<br>1   | GAC<br>Asp | TAT<br>Tyr        | CAA<br>Gln        | GTG<br>Val<br>5   | TCA<br>Ser        | AGT<br>Ser        | CCA<br>Pro        | ACC<br>Thr        | TAT<br>Tyr<br>10  | GAC<br>Asp        | ATC<br>Ile        | GAT<br>Asp        | TAT<br>Tyr<br>15  | TAT<br>Tyr<br>15  | ACA<br>Thr        | 48  |
| TCG<br>Ser        | GAA<br>Glu | CCC<br>Pro        | TGC<br>Cys<br>20  | CAA<br>Gln        | AAA<br>Lys        | ATC<br>Ile        | AAT<br>Asn        | GTG<br>Val<br>25  | AAA<br>Lys        | CAA<br>Gln        | ATC<br>Ile        | GCA<br>Ala        | GCC<br>Ala<br>30  | CGC<br>Arg        | CTC<br>Leu        | 96  |
| CTG<br>Leu        | CCT<br>Pro | CCG<br>Pro<br>35  | CTC<br>Leu        | TAC<br>Tyr        | TCA<br>Ser        | CTG<br>Leu        | GTG<br>Val<br>40  | TTC<br>Phe        | ATC<br>Ile        | TTT<br>Phe        | GGT<br>Gly        | TTT<br>Phe<br>45  | GTG<br>Val        | GGC<br>Gly        | AAC<br>Asn        | 144 |
| ATA<br>Ile<br>50  | CTG<br>Leu | GTC<br>Val        | GTC<br>Val        | CTC<br>Leu        | ATC<br>Ile        | CTG<br>Leu<br>55  | ATA<br>Ile        | AAC<br>Asn        | TGC<br>Cys        | AAA<br>Lys        | AGG<br>Arg<br>60  | CTG<br>Leu        | AAA<br>Lys        | AGC<br>Ser        | ATG<br>Met        | 192 |
| ACT<br>Thr<br>65  | GAC<br>Asp | ATC<br>Ile        | TAC<br>Tyr        | CTG<br>Leu        | CTC<br>Leu<br>70  | AAC<br>Asn        | CTG<br>Leu        | GCC<br>Ala        | ATC<br>Ile        | TCT<br>Ser<br>75  | GAC<br>Asp        | CTG<br>Leu        | CTT<br>Leu        | TTC<br>Phe        | CTT<br>Leu<br>80  | 240 |
| CTT<br>Leu        | ACT<br>Thr | GTC<br>Val        | CCC<br>Pro        | TTC<br>Phe<br>85  | TGG<br>Trp        | GCT<br>Ala        | CAC<br>His        | TAT<br>Tyr<br>90  | GCT<br>Ala        | GCT<br>Ala        | GCC<br>Ala        | CAG<br>Gln        | TGG<br>Trp        | GAC<br>Asp<br>95  | TTT<br>Phe        | 288 |
| GGA<br>Gly        | AAT<br>Asn | ACA<br>Thr        | ATG<br>Met<br>100 | TGT<br>Cys        | CAA<br>Gln        | CTC<br>Leu        | TTG<br>Leu<br>105 | ACA<br>Thr        | GGG<br>Gly        | CTC<br>Leu        | TAT<br>Tyr        | TTT<br>Phe<br>110 | ATA<br>Ile        | GGC<br>Gly        | TTC<br>Phe        | 336 |
| TTC<br>Phe        | TCT<br>Ser | GGA<br>Gly<br>115 | ATC<br>Ile        | TTC<br>Phe        | TTC<br>Phe        | ATC<br>Ile        | ATC<br>Ile<br>120 | CTC<br>Leu        | CTG<br>Leu        | ACA<br>Thr        | ATC<br>Ile        | GAT<br>Asp<br>125 | AGG<br>Arg        | TAC<br>Tyr        | CTG<br>Leu        | 384 |
| GCT<br>Ala<br>130 | ATC<br>Ile | GTC<br>Val        | CAT<br>His        | GCT<br>Ala        | GTG<br>Val        | TTT<br>Phe<br>135 | GCT<br>Ala        | TTA<br>Leu        | AAA<br>Lys        | GCC<br>Ala        | AGG<br>Arg<br>140 | ACA<br>Thr        | GTC<br>Val        | ACC<br>Thr        | TTT<br>Phe        | 432 |
| GGG<br>Gly<br>145 | GTG<br>Val | GTG<br>Val        | ACA<br>Thr        | AGT<br>Ser        | GTG<br>Val<br>150 | ATC<br>Ile        | ACT<br>Thr        | TGG<br>Trp        | GTG<br>Val        | GTG<br>Val        | GCT<br>Ala        | GTG<br>Val        | TTT<br>Phe        | GCC<br>Ala        | TCT<br>Ser<br>160 | 480 |
| CTC<br>Leu        | CCA<br>Pro | GGA<br>Gly        | ATC<br>Ile        | ATC<br>Ile        | TTT<br>Phe<br>165 | ACC<br>Thr        | AGA<br>Arg        | TCT<br>Ser        | CAG<br>Gln        | AGA<br>Arg        | GAA<br>Glu        | GGT<br>Gly        | CTT<br>Leu        | CAT<br>His<br>175 | TAC<br>Tyr        | 528 |
| ACC<br>Thr        | TGC<br>Cys | AGC<br>Ser        | TCT<br>Ser        | CAT<br>His        | TTT<br>Phe<br>180 | CCA<br>Pro        | TAC<br>Tyr        | AGT<br>Ser<br>185 | CAG<br>Gln        | TAT<br>Tyr        | CAA<br>Gln        | TTC<br>Phe        | TGG<br>Trp<br>190 | AAG<br>Lys        | AAT<br>Asn        | 576 |
| TTT<br>Phe        | CAG<br>Gln | ACA<br>Thr<br>195 | TTA<br>Leu        | AAG<br>Lys        | ATG<br>Met        | GTC<br>Val        | ATC<br>Ile<br>200 | TTG<br>Leu        | GGG<br>Gly        | CTG<br>Leu        | GTC<br>Val        | CTG<br>Leu        | CCG<br>Pro        | CTG<br>Leu        | CTT<br>Leu        | 624 |
| GTC<br>Val<br>210 | ATG<br>Met | GTC<br>Val        | ATC<br>Ile        | TGC<br>Cys        | TAC<br>Tyr        | TCG<br>Ser<br>215 | GGA<br>Gly        | ATC<br>Ile        | CTG<br>Leu        | AAA<br>Lys        | ACT<br>Thr<br>220 | CTG<br>Leu        | CTT<br>Leu        | CGG<br>Arg        | TGT<br>Cys        | 672 |
| CGA<br>Arg<br>225 | AAC<br>Asn | GAG<br>Glu        | AAG<br>Lys        | AAG<br>Lys        | AGG<br>Arg<br>230 | CAC<br>His        | AGG<br>Arg        | GCT<br>Ala        | GTG<br>Val        | AGG<br>Arg<br>235 | CTT<br>Leu        | ATC<br>Ile        | TTC<br>Phe        | ACC<br>Thr        | ATC<br>Ile<br>240 | 720 |
| ATG<br>Met        | ATT<br>Ile | GTT<br>Val        | TAT<br>Tyr        | TTT<br>Phe<br>245 | CTC<br>Leu        | TTG<br>Leu        | TGG<br>Trp        | GCT<br>Ala        | CCC<br>Pro<br>250 | TAC<br>Tyr        | AAC<br>Asn        | ATT<br>Ile        | GTC<br>Val        | CTT<br>Leu<br>255 | CTC<br>Leu        | 768 |
| CTG<br>Leu        | AAC<br>Asn | ACC<br>Thr        | TTC<br>Phe<br>260 | CAG<br>Gln        | GAA<br>Glu        | TTC<br>Phe        | TTT<br>Phe        | GGC<br>Gly<br>265 | CTG<br>Leu        | AAT<br>Asn        | AAT<br>Asn        | TGC<br>Cys        | AGT<br>Ser        | AGC<br>Ser        | TCT<br>Ser        | 816 |

|   |      |
|---|------|
| AAC AGG TTG GAC CAA GCC ATG CAG GTG ACA GAG ACT CTT GGG ATG ACA | 864  |
| Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr |      |
| 275 280 285   |      |
| CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC | 912  |
| His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe |      |
| 290 295 300   |      |
| AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC | 960  |
| Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe |      |
| 305 310 315 320   |      |
| TGC AAA TGC TGT TCC ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGT | 1008 |
| Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser |      |
| 325 330 335   |      |
| TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG | 1056 |
| Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu |      |
| 340 345 350   |      |
| TGA   | 1059 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|   |  |
|---|--|
| Met Asp Tyr Gln Val Ser Ser Pro Thr Tyr Asp Ile Asp Tyr Tyr Thr |  |
| 1 5 10 15   |  |
| Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu |  |
| 20 25 30  |  |
| Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn |  |
| 35 40 45  |  |
| Ile Leu Val Val Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met |  |
| 50 55 60  |  |
| Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu |  |
| 65 70 75 80   |  |
| Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe |  |
| 85 90 95  |  |
| Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe |  |
| 100 105 110   |  |
| Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu |  |
| 115 120 125   |  |
| Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe |  |
| 130 135 140   |  |
| Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser |  |
| 145 150 155 160   |  |
| Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Arg Glu Gly Leu His Tyr |  |
| 165 170 175   |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Ser | Ser | His | Phe | Pro | Tyr | Ser | Gln | Tyr | Gln | Phe | Trp | Lys | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Gln | Thr | Leu | Lys | Met | Val | Ile | Leu | Gly | Leu | Val | Leu | Pro | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Met | Val | Ile | Cys | Tyr | Ser | Gly | Ile | Leu | Lys | Thr | Leu | Leu | Arg | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Asn | Glu | Lys | Lys | Arg | His | Arg | Ala | Val | Arg | Leu | Ile | Phe | Thr | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Ile | Val | Tyr | Phe | Leu | Leu | Trp | Ala | Pro | Tyr | Asn | Ile | Val | Leu | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Asn | Thr | Phe | Gln | Glu | Phe | Phe | Gly | Leu | Asn | Asn | Cys | Ser | Ser | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Arg | Leu | Asp | Gln | Ala | Met | Gln | Val | Thr | Glu | Thr | Leu | Gly | Met | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Cys | Cys | Ile | Asn | Pro | Ile | Ile | Tyr | Ala | Phe | Val | Gly | Glu | Lys | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Asn | Tyr | Leu | Leu | Val | Phe | Phe | Gln | Lys | His | Ile | Ala | Lys | Arg | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Cys | Lys | Cys | Cys | Ser | Ile | Phe | Gln | Gln | Glu | Ala | Pro | Glu | Arg | Ala | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Val | Tyr | Thr | Arg | Ser | Thr | Gly | Glu | Gln | Glu | Ile | Ser | Val | Gly | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |